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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=11; day=25; hr=15; min=39; sec=32; ms=339;  
]

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Application No: 10582987

Version No: 1.0

Input Set:

Output Set:

Started: 2007-11-02 19:48:49.494

Finished: 2007-11-02 19:48:51.858

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 364 ms

Total Warnings: 28

Total Errors: 0

No. of SeqIDs Defined: 30

Actual SeqID Count: 30

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
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W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

**Input Set:**

**Output Set:**

**Started:** 2007-11-02 19:48:49.494  
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**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 364 ms  
**Total Warnings:** 28  
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**No. of SeqIDs Defined:** 30  
**Actual SeqID Count:** 30

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

# SEQUENCE LISTING

<110> Patrice Jacques Marie PELLERIN  
Bruno BLONDIN  
Jean-Marie SABLAYROLLES  
Carole GUILLAME

<120> YEAST STRAINS WITH IMPROVED FRUCTOSE FERMENTATION CAPACITY

<130> 4662-194 / 21568USWO

<140> 10582987

<141> 2007-11-02

<150> PCT/EP2004/014577

<151> 2004-12-20

<150> EP 03078992.9

<151> 2003-12-19

<160> 30

<170> MS Word

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<223> primer

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<213> Artificial Sequence

<220>

<223> primer

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<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

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<210> 24

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

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<210> 25

<211> 1704

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 25

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actgtgtcta tctgttgtgt tatgggtgcc ttcgggtggt tcgttttcgg ttgggatact	240
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aaagatggta gttattatth gtctaagggt agaactgggt taattgtctc cattttcaac	360
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gcctgggctt tgtttatgat cgggtggtatg actttcgttc cagaatcccc acgttatthg	780
gttgaagctg gtcaaatgta cgaagcaaga gcatctctth ccaaagttaa caagggtgcc	840
ccagaccatc cattcattca acaagagttg gaagttatth aagctagtgt tgaagaagct	900
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cgtactatga tgggtatcat gatccaatct ctacaacaat tgactggtga taactatthc	1020
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aagaaaatgt tcggcaagaa ataa 1704

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<210> 26
<211> 567
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 26

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1           5           10           15

```

```

Ser Asn Ala Asp Leu Pro Ser Asn Ser Ser Gln Val Met Asn Met Pro
          20           25           30

```

```

Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
          35           40           45

```

```

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
          50           55           60

```

```

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
65           70           75           80

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```

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
          85           90           95

```

```

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
          100          105          110

```

```

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
          115          120          125

```

```

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
          130          135          140

```

```

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
          145          150          155          160

```

```

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
          165          170          175

```

```

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
          180          185          190

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Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met

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Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe					
225		230		235	240
Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser					
	245		250		255
Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser					
	260		265		270
Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln					
	275		280		285
Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly					
	290		295		300
Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys					
305		310		315	320
Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly					
	325		330		335
Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly					
	340		345		350
Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe					
	355		360		365
Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg					
	370		375		380
Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val					
385		390		395	400
Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn					
	405		410		415
Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe					
	420		425		430
Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val					
	435		440		445
Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile					
	450		455		460
Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr					
465		470		475	480
Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met					
	485		490		495
Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu					

500	505	510
Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly		
515	520	525
Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly		
530	535	540
Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr		
545	550	555
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Lys Lys Met Phe Gly Lys Lys		
	565	

<210> 27

<211> 567

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated HXT3 protein

<400> 27

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Ser Asn Ala Asp Leu Pro Ser Asn Ser Ser Gln Val Met Asn Met Pro		
	20	25
		30
Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val		
	35	40
		45
Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile		
	50	55
		60
Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr		
65	70	75
		80
Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe		
	85	90
		95
Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr		
	100	105
		110
Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile		
	115	120
		125
Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile		
	130	135
		140
Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser		
145	150	155
		160
Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu		
	165	170
		175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val	180	185	190
Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met	195	200	205
Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys	210	215	220
Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe	225	230	235
Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser	245	250	255
Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser	260	265	270
Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln	275	280	285
Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly	290	295	300
Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys	305	310	315
Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly	325	330	335
Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly	340	345	350
Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe	355	360	365
Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg	370	375	380
Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val	385	390	395
Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn	405	410	415
Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe	420	425	430
Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val	435	440	445
Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile	450	455	460
Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr	465	470	475
			480

Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met  
485 490 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu  
500 505 510

Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly  
515 520 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly  
530 535 540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr  
545 550 555 560

Lys Lys Met Phe Gly Lys Lys  
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<210> 28

<211> 1704

<212> DNA

<213> Artificial Sequence

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<223> mutated HXT3 gene

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actgtgtcta	tctgttgtgt	tatggttgcc	ttcgggtggt	tcgttttcgg	ttgggataact	240
gggtaccattt	ctgggttcgt	cgcctcaact	gatttcttga	gaagattcgg	tatgaagcat	300
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atgggtttga	ttgtcgttgt	tggtatctac	atcatcggtg	ttattattca	aattgcatcc	480
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